

SEQUENCE LISTING

<110>KAO CORPORATION

<120>New mutant alpha-amylase


<130>

<150>JP P1999-163569

<151>1999-06-10

<160>23

<210>1

<211>480

<212>PRT

<213>Bacillus sp. KSM-K38

<400>1

Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu

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Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu

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30

Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly

35

40

45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu

50	55	60
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys		
65	70	75
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn		
85	90	95
Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr		
100	105	110
Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp		
115	120	125
Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser		
130	135	140
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe		
145	150	155
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg		
165	170	175
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn		
180	185	190
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val		
195	200	205
Gln Asp Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp		
210	215	220
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr		
225	230	235
Thr Ser Asp Trp Val Arg His Gln Arg Asn Glu Ala Asp Gln Asp Leu		
245	250	255
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe		

260 265 270
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
275 280 285
Asn Tyr Asn Phe Tyr Arg Ala Ser Gln Gln Gly Gly Ser Tyr Asp Met
290 295 300
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Met His Ala
305 310 315 320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu
325 330 335
Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
340 345 350
Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
355 360 365
Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
370 375 380
Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385 390 395 400
Asp His Trp Asp Val Val Gly Trp Thr Arg Glu Gly Ser Ser Ser Arg
405 410 415
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430
Lys Trp Met Tyr Val Gly Arg Gln Asn Ala Gly Gln Thr Trp Thr Asp
435 440 445
Leu Thr Gly Asn Asn Gly Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
450 455 460
Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln

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<212>PRT

<213>Bacillus sp. KSM-AP1378

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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala

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30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp

35

40

45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr

50

55

60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly

65

70

75

80

Thr Arg Ser Gln Leu Gln Gly Ala Val Thr Ser Leu Lys Asn Asn Gly

85

90

95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp

100

105

110

Gly Thr Glu Met Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn

115

120

125

Gln Glu Ile Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp

130

135

140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145 150 155 160
His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
165 170 175
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190
Ile Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205
Asp His Pro Glu Val Ile Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220
Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240
Ile Lys Tyr Ser Tyr Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
245 250 255
Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270
Ala Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
275 280 285
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
290 295 300
Gly Tyr Phe Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305 310 315 320
His Pro Ile His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335
Gly Glu Ala Leu Glu Ser Phe Val Gln Ser Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Ile Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ser Met Lys Ser
370 375 380
Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Tyr Ala Tyr Gly Thr
385 390 395 400
Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415
Gly Asp Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430
Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys His Lys Ala Gly
435 440 445
Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Ser Gly Thr Val Thr Ile
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Asn Ala Asp Gly Trp Gly Asn Phe Thr Val Asn Gly Gly Ala Val Ser
465 470 475 480
Val Trp Val Lys Gln
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<213>Bacillus sp. KSM-K38

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<222>(162)..(224)

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<222>(225)..(1664)

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<222>(162)..(1664)

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ttatgatata tgtaagcgtt atcattaaaa ggaggtatTT g atg aga aga tgg gta 176
gta gca atg ttg gca gtg tta ttt tta ttt cct tcg gta gta gtt gca 224
gat gga ttg aac ggt acg atg atg cag tat tat gag tgg cat ttg gaa 272
Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
1 5 10 15
aac gac ggg cag cat tgg aat cgg ttg cac gat gat gcc gca gct ttg 320
Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Ala Ala Leu
20 25 30
agt gat gct ggt att aca gct att tgg att ccg cca gcc tac aaa ggt 368
Ser Asp Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45
aat agt cag gcg gat gtt ggg tac ggt gca tac gat ctt tat gat tta 416
Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu

50	55	60	
gga gag ttc aat caa aag ggt act gtt cga acg aaa tac gga act aag			464
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys			
65	70	75	80
gca cag ctt gaa cga gct att ggg tcc ctt aaa tct aat gat atc aat			512
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn			
85	90	95	
gta tac gga gat gtc gtg atg aat cat aaa atg gga gct gat ttt acg			560
Val Tyr Gly Asp Val Val Met Asn His Lys Met Gly Ala Asp Phe Thr			
100	105	110	
gag gca gtg caa gct gtt caa gta aat cca acg aat cgt tgg cag gat			608
Glu Ala Val Gln Ala Val Gln Val Asn Pro Thr Asn Arg Trp Gln Asp			
115	120	125	
att tca ggt gcc tac acg att gat gcg tgg acg ggt ttc gac ttt tca			656
Ile Ser Gly Ala Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Ser			
130	135	140	
ggg cgt aac aac gcc tat tca gat ttt aag tgg aga tgg ttc cat ttt			704
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe			
145	150	155	160
aat ggt gtt gac tgg gat cag cgc tat caa gaa aat cat att ttc cgc			752
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Ile Phe Arg			
165	170	175	
ttt gca aat acg aac tgg aac tgg cga gtg gat gaa gag aac ggt aat			800
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn			
180	185	190	
tat gat tac ctg tta gga tcg aat atc gac ttt agt cat cca gaa gta			848

Tyr	Asp	Tyr	Leu	Leu	Gly	Ser	Asn	Ile	Asp	Phe	Ser	His	Pro	Glu	Val	
195									200					205		
caa	gat	gag	ttg	aag	gat	tgg	ggt	agc	tgg	ttt	acc	gat	gag	tta	gat	896
Gln	Asp	Glu	Leu	Lys	Asp	Trp	Gly	Ser	Trp	Phe	Thr	Asp	Glu	Leu	Asp	
210								215					220			
ttg	gat	ggt	tat	cgt	tta	gat	gct	att	aaa	cat	att	cca	ttc	tgg	tat	944
Leu	Asp	Gly	Tyr	Arg	Leu	Asp	Ala	Ile	Lys	His	Ile	Pro	Phe	Trp	Tyr	
225					230					235			240			
aca	tct	gat	tgg	gtt	cgg	cat	cag	cgc	aac	gaa	gca	gat	caa	gat	tta	992
Thr	Ser	Asp	Trp	Val	Arg	His	Gln	Arg	Asn	Glu	Ala	Asp	Gln	Asp	Leu	
245					250					255						
ttt	gtc	gta	ggg	gaa	tat	tgg	aag	gat	gac	gta	ggt	gct	ctc	gaa	ttt	1040
Phe	Val	Val	Gly	Glu	Tyr	Trp	Lys	Asp	Asp	Val	Gly	Ala	Leu	Glu	Phe	
260					265					270						
tat	tta	gat	gaa	atg	aat	tgg	gag	atg	tct	cta	ttc	gat	gtt	cca	ctt	1088
Tyr	Leu	Asp	Glu	Met	Asn	Trp	Glu	Met	Ser	Leu	Phe	Asp	Val	Pro	Leu	
275					280					285						
aat	aat	aat	ttt	tac	cgg	gct	tca	caa	caa	ggt	gga	agc	tat	gat	atg	1136
Asn	Tyr	Asn	Phe	Tyr	Arg	Ala	Ser	Gln	Gln	Gly	Gly	Ser	Tyr	Asp	Met	
290					295					300						
cgt	aat	att	tta	cga	gga	tct	tta	gta	gaa	gcg	cat	ccg	atg	cat	gca	1184
Arg	Asn	Ile	Leu	Arg	Gly	Ser	Leu	Val	Glu	Ala	His	Pro	Met	His	Ala	
305					310					315			320			
gtt	acg	ttt	gtt	gat	aat	cat	gat	act	cag	cca	ggg	gag	tca	tta	gag	1232
Val	Thr	Phe	Val	Asp	Asn	His	Asp	Thr	Gln	Pro	Gly	Glu	Ser	Leu	Glu	
325					330					335						

tca	tgg	gtt	gct	gat	tgg	ttt	aag	cca	ctt	gct	tat	gcg	aca	att	ttg	1280
Ser	Trp	Val	Ala	Asp	Trp	Phe	Lys	Pro	Leu	Ala	Tyr	Ala	Thr	Ile	Leu	
340															350	
acg	cgt	gaa	ggt	ggt	tat	cca	aat	gta	ttt	tac	ggt	gat	tac	tat	ggg	1328
Thr	Arg	Glu	Gly	Gly	Tyr	Pro	Asn	Val	Phe	Tyr	Gly	Asp	Tyr	Tyr	Gly	
355															365	
att	cct	aac	gat	aac	att	tca	gct	aaa	aaa	gat	atg	att	gat	gag	ctg	1376
Ile	Pro	Asn	Asp	Asn	Ile	Ser	Ala	Lys	Lys	Asp	Met	Ile	Asp	Glu	Leu	
370															380	
ctt	gat	gca	cgt	caa	aat	tac	gca	tat	ggc	acg	cag	cat	gac	tat	ttt	1424
Leu	Asp	Ala	Arg	Gln	Asn	Tyr	Ala	Tyr	Gly	Thr	Gln	His	Asp	Tyr	Phe	
385															400	
gat	cat	tgg	gat	gtt	gta	gga	tgg	act	agg	gaa	gga	tct	tcc	tcc	aga	1472
Asp	His	Trp	Asp	Val	Val	Gly	Trp	Thr	Arg	Glu	Gly	Ser	Ser	Ser	Arg	
405															415	
cct	aat	tca	ggc	ctt	gct	act	att	atg	tcg	aat	gga	cct	ggt	ggt	tcc	1520
Pro	Asn	Ser	Gly	Leu	Ala	Thr	Ile	Met	Ser	Asn	Gly	Pro	Gly	Gly	Ser	
420															430	
aag	tgg	atg	tat	gta	gga	cgt	cag	aat	gca	gga	caa	aca	tgg	aca	gat	1568
Lys	Trp	Met	Tyr	Val	Gly	Arg	Gln	Asn	Ala	Gly	Gln	Thr	Trp	Thr	Asp	
435															445	
tta	act	ggt	aat	aac	gga	gct	tcc	gtt	aca	att	aat	ggt	gat	gga	tgg	1616
Leu	Thr	Gly	Asn	Asn	Gly	Ala	Ser	Val	Thr	Ile	Asn	Gly	Asp	Gly	Trp	
450															460	
ggc	gaa	tcc	ttt	acg	aat	gga	gga	tct	gta	tcc	gtg	tac	gtg	aac	caa	1664

Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
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<212>PRT

<213>Bacillus sp. KSM-K36

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Asp Gly Leu Asn Gly Thr Met Met Gln Tyr Tyr Glu Trp His Leu Glu
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Asn Asp Gly Gln His Trp Asn Arg Leu His Asp Asp Ala Glu Ala Leu
20 25 30

Ser Asn Ala Gly Ile Thr Ala Ile Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Asn Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Met Asn His Lys Leu Gly Ala Asp Phe Thr
100 105 110

Glu Ala Val Gln Ala Val Gln Val Asn Pro Ser Asn Arg Trp Gln Asp

115 120 125
Ile Ser Gly Val Tyr Thr Ile Asp Ala Trp Thr Gly Phe Asp Phe Pro
130 135 140
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp Phe His Phe
145 150 155 160
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His Leu Phe Arg
165 170 175
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu Glu Asn Gly Asn
180 185 190
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His Pro Glu Val
195 200 205
Gln Glu Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp
210 215 220
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr
225 230 235 240
Thr Ser Asp Trp Val Arg His Gln Arg Ser Glu Ala Asp Gln Asp Leu
245 250 255
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe
260 265 270
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu
275 280 285
Asn Tyr Asn Phe Tyr Arg Ala Ser Lys Gln Gly Gly Ser Tyr Asp Met
290 295 300
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Ile His Ala
305 310 315 320
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu

325 330 335
Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
340 345 350
Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
355 360 365
Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
370 375 380
Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
385 390 395 400
Asp His Trp Asp Ile Val Gly Trp Thr Arg Glu Gly Thr Ser Ser Arg
405 410 415
Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
420 425 430
Lys Trp Met Tyr Val Gly Gln Gln His Ala Gly Gln Thr Trp Thr Asp
435 440 445
Leu Thr Gly Asn His Ala Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
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Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
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<211>1625

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<213>Bacillus sp. KSM-K36

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<222>(40)..(102)

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gat	ggc	ttg	aat	gga	acg	atg	atg	cag	tat	tat	gag	tgg	cat	cta	gag	150
Asp	Gly	Leu	Asn	Gly	Thr	Met	Met	Gln	Tyr	Tyr	Glu	Trp	His	Leu	Glu	
1	5					10							15			
aat	gat	ggg	caa	cac	tgg	aat	cgg	ttg	cat	gat	gat	gcc	gaa	gct	tta	198
Asn	Asp	Gly	Gln	His	Trp	Asn	Arg	Leu	His	Asp	Asp	Ala	Glu	Ala	Leu	
20	25					30										
agt	aat	gct	ggt	att	aca	gct	att	tgg	ata	ccc	cca	gcc	tac	aaa	gga	246
Ser	Asn	Ala	Gly	Ile	Thr	Ala	Ile	Trp	Ile	Pro	Pro	Ala	Tyr	Lys	Gly	
35	40					45										
aat	agt	cag	gct	gat	gtt	ggg	tat	ggt	gca	tac	gac	ctt	tat	gat	tta	294
Asn	Ser	Gln	Ala	Asp	Val	Gly	Tyr	Gly	Ala	Tyr	Asp	Leu	Tyr	Asp	Leu	
50	55					60										

ggg gag ttt aat caa aaa ggt acc gtt cga acg aaa tac	ggg aca aag	342
Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr	Gly Thr Lys	
65	70	75
gct cag ctt gag cga gct ata ggg tcc cta aag tcg aat	aat gat atc aat	390
Ala Gln Leu Glu Arg Ala Ile Gly Ser Leu Lys Ser Asn	Asp Ile Asn	
	85	90
gtt tat ggg gat gtc gta atg aat cat aaa tta gga gct	aat gat ttc acg	438
Val Tyr Gly Asp Val Val Met Asn His Lys Leu Gly Ala	Asp Phe Thr	
100	105	110
gag gca gtg caa gct gtt caa gta aat cct tcg aac cgt	tgg cag gat	486
Glu Ala Val Gln Ala Val Gln Val Asn Pro Ser Asn Arg	Trp Gln Asp	
115	120	125
att tca ggt gtc tac acg att gat gca tgg acg gga	ttt gac ttt cca	534
Ile Ser Gly Val Tyr Thr Ile Asp Ala Trp Thr Gly Phe	Asp Pro	
130	135	140
ggg cgc aac aat gcc tat tcc gat ttt aaa tgg aga tgg	ttc cat ttt	582
Gly Arg Asn Asn Ala Tyr Ser Asp Phe Lys Trp Arg Trp	Phe His Phe	
145	150	155
aat ggc gtt gac tgg gat caa cgc tat caa gaa aac	cat ctt ttt cgc	630
Asn Gly Val Asp Trp Asp Gln Arg Tyr Gln Glu Asn His	Leu Phe Arg	
165	170	175
ttt gca aat acg aac tgg aac tgg cga gtg gat gaa	gag aat ggt aat	678
Phe Ala Asn Thr Asn Trp Asn Trp Arg Val Asp Glu	Glu Asn Gly Asn	
180	185	190
tat gac tat tta tta gga tcg aac att gac ttt agc	cac cca gag gtt	726
Tyr Asp Tyr Leu Leu Gly Ser Asn Ile Asp Phe Ser His	Pro Glu Val	

195	200	205	
caa gag gaa tta aag gat tgg ggg agc tgg ttt acg gat gag cta gat			774
Gln Glu Glu Leu Lys Asp Trp Gly Ser Trp Phe Thr Asp Glu Leu Asp			
210	215	220	
tta gat ggg tat cga ttg gat gct att aag cat att cca ttc tgg tat			822
Leu Asp Gly Tyr Arg Leu Asp Ala Ile Lys His Ile Pro Phe Trp Tyr			
225	230	235	240
acg tca gat tgg gtt agg cat cag cga agt gaa gca gac caa gat tta			870
Thr Ser Asp Trp Val Arg His Gln Arg Ser Glu Ala Asp Gln Asp Leu			
245	250	255	
ttt gtc gta ggg gag tat tgg aag gat gac gta ggt gct ctc gaa ttt			918
Phe Val Val Gly Glu Tyr Trp Lys Asp Asp Val Gly Ala Leu Glu Phe			
260	265	270	
tat tta gat gaa atg aat tgg gag atg tct cta ttc gat gtt ccg ctc			966
Tyr Leu Asp Glu Met Asn Trp Glu Met Ser Leu Phe Asp Val Pro Leu			
275	280	285	
aat tat aat ttt tac cgg gct tca aag caa ggc gga agc tat gat atg			1014
Asn Tyr Asn Phe Tyr Arg Ala Ser Lys Gln Gly Gly Ser Tyr Asp Met			
290	295	300	
cgt aat att tta cga gga tct tta gta gaa gca cat ccg att cat gca			1062
Arg Asn Ile Leu Arg Gly Ser Leu Val Glu Ala His Pro Ile His Ala			
305	310	315	320
gtt acg ttt gtt gat aat cat gat act cag cca gga gag tca tta gaa			1110
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Glu Ser Leu Glu			
325	330	335	
tca tgg gtc gct gat tgg ttt aag cca ctt gct tat gcg aca atc ttg			1158

Ser Trp Val Ala Asp Trp Phe Lys Pro Leu Ala Tyr Ala Thr Ile Leu
 340 345 350
 acg cgt gaa ggt ggt tat cca aat gta ttt tac ggt gac tac tat ggg 1206
 Thr Arg Glu Gly Gly Tyr Pro Asn Val Phe Tyr Gly Asp Tyr Tyr Gly
 355 360 365
 att cct aac gat aac att tca gct aag aag gat atg att gat gag ttg 1254
 Ile Pro Asn Asp Asn Ile Ser Ala Lys Lys Asp Met Ile Asp Glu Leu
 370 375 380
 ctt gat gca cgt caa aat tac gca tat ggc aca caa cat gac tat ttt 1302
 Leu Asp Ala Arg Gln Asn Tyr Ala Tyr Gly Thr Gln His Asp Tyr Phe
 385 390 395 400
 gat cat tgg gat atc gtt gga tgg aca aga gaa ggt aca tcc tca cgt 1350
 Asp His Trp Asp Ile Val Gly Trp Thr Arg Glu Gly Thr Ser Ser Arg
 405 410 415
 cct aat tcg ggt ctt gct act att atg tcc aat ggt cct gga gga tca 1398
 Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asn Gly Pro Gly Gly Ser
 420 425 430
 aaa tgg atg tac gta gga cag caa cat gca gga caa acg tgg aca gat 1446
 Lys Trp Met Tyr Val Gly Gln Gln His Ala Gly Gln Thr Trp Thr Asp
 435 440 445
 tta act ggc aat cac gcg gcg tcg gtt acg att aat ggt gat ggc tgg 1494
 Leu Thr Gly Asn His Ala Ala Ser Val Thr Ile Asn Gly Asp Gly Trp
 450 455 460
 ggc gaa ttc ttt aca aat gga gga tct gta tcc gtg tat gtg aac caa 1542
 Gly Glu Phe Phe Thr Asn Gly Gly Ser Val Ser Val Tyr Val Asn Gln
 465 470 475 480

taataaaaag ccttgagaag ggatccctcc ctaactcaag gctttttta tgtcgtttag 1602
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<211>30

<212>DNA

<213>Artificial Sequence

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